

(2)

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/849,869

DATE: 05/17/2001

TIME: 08:54:44

Input Set : A:\CALTE004C1seqlist.txt
 Output Set: N:\CRF3\05172001\I849869.raw

4 <110> APPLICANT: Anderson, David J.
 5 Dong, Xinzhang
 6 Zylka, Mark
 7 Simon, Melvin
 8 Han, Sang-kyou
 10 <120> TITLE OF INVENTION: PAIN SIGNALING MOLECULES
 13 <130> FILE REFERENCE: CALTE.004C1
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/849,869
 C--> 15 <141> CURRENT FILING DATE: 2001-05-04
 15 <150> PRIOR APPLICATION NUMBER: US 60/222,344
 16 <151> PRIOR FILING DATE: 2000-08-01
 18 <150> PRIOR APPLICATION NUMBER: US 60/202,027
 19 <151> PRIOR FILING DATE: 2000-05-04
 21 <150> PRIOR APPLICATION NUMBER: US 09/704,707
 22 <151> PRIOR FILING DATE: 2000-11-03
 24 <150> PRIOR APPLICATION NUMBER: US unknown
 25 <151> PRIOR FILING DATE: 2001-04-19
 27 <160> NUMBER OF SEQ ID NOS: 109
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1088
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Mus Musculus
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (115)...(1026)
 40 <400> SEQUENCE: 1
 41 acagaaggcca gagagctaca tccagcaaga ggaatggggg aaagcagcac ctgtgcaggg 60
 42 tttctagccc taaacacatc ggcctcgcca acagcacccca caacaactaa tcca atg 117
 43 Met
 44 1
 46 gac aat acc atc cct gga ggt atc aac atc acg att ctg atc cca aac 165
 47 Asp Asn Thr Ile Pro Gly Gly Ile Asn Ile Thr Ile Leu Ile Pro Asn
 48 5 10 15
 50 ttg atg atc atc atc ttc gga ctg gtc ggg ctg aca gga aat ggc att 213
 51 Leu Met Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly Ile
 52 20 25 30
 54 gtg ttc tgg ctc ctg ggc ttc tgt ctg cac agg aac gcc ttc tca gtc 261
 55 Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser Val
 56 35 40 45
 58 tac atc cta aac tta gct cta gct gac ttc ttc ctc cta ggt cac 309
 59 Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly His
 60 50 55 60 65
 62 atc ata gat tcc ata ctg ctt ctt ctc aat gtt ttc tac cca att acc 357
 63 Ile Ile Asp Ser Ile Leu Leu Leu Asn Val Phe Tyr Pro Ile Thr
 64 70 75 80
 66 ttt ctc ttg tgc ttt tac acg atc atg gtt ctc tat atc gca ggc 405

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67 Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala Gly
 68 85 90 95
 70 ctg agc atg ctc agt gcc atc agc act gag cgc tgc ctg tct gta ctg 453
 71 Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu
 72 100 105 110
 74 tgc ccc atc tgg tat cac tgt cac cgc cca gaa cac aca tca act gtc 501
 75 Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr Val
 76 115 120 125
 78 atg tgt gct gtc atc tgg gtc ctg tcc ctg ttg atc tgc att ctg aat 549
 79 Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile Leu Asn
 80 130 135 140 145
 82 agt tat ttc tgc ggt ttc tta aat acc caa tat aaa aat gaa aat ggg 597
 83 Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn Gly
 84 150 155 160
 86 tgt ctg gca ttg aac ttc ttt act gct gca tac ctg atg ttt ttg ttt 645
 87 Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu Phe
 88 165 170 175
 90 gtg gtc ctc tgt ctg tcc agc ctg gct ctg gtg gcc agg ttg ttc tgt 693
 91 Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe Cys
 92 180 185 190
 94 ggt act ggg cag ata aag ctt acc aga ttg tat gta acc att att ctg 741
 95 Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile Leu
 96 195 200 205
 98 agc att ttg gtt ttt ctc ctt tgc gga ttg ccc ttt ggc atc cac tgg 789
 99 Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His Trp
 100 210 215 220 225
 102 ttt ctg tta ttc aag att aag gat gat ttt cat gta ttt gat ctt gga 837
 103 Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu Gly
 104 230 235 240
 106 ttt tat ctg gca tca gtt gtc ctg act gct att aat agc tgt gcc aac 885
 107 Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala Asn
 108 245 250 255
 110 ccc atc att tac ttc ttc gtg gga tcc ttc agg cat cgg ttg aag cac
 111 Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys His
 112 260 265 270
 114 cag acc ctc aaa atg gtt ctc cag aat gca ctg caa gac act cct gag 981
 115 Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro Glu
 116 275 280 285
 118 aca gcc aaa atc atg gtg gag atg tca aga agc aaa tca gag cca 1026
 119 Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
 120 290 295 300
 122 tgatgaagag cctttgcctg gcccttagaa gtggctttgg ggtgagcatt gccctgtgc 1086
 123 ac 1088
 125 <210> SEQ ID NO: 2
 126 <211> LENGTH: 304
 127 <212> TYPE: PRT
 128 <213> ORGANISM: Mus Musculus
 130 <400> SEQUENCE: 2
 131 Met Asp Asn Thr Ile Pro Gly Gly Ile Asn Ile Thr Ile Leu Ile Pro

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Input Set : A:\CALTE004C1seqlist.txt

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132 1 5 10 15
 133 Asn Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Thr Gly Asn Gly
 134 20 25 30
 135 Ile Val Phe Trp Leu Leu Gly Phe Cys Leu His Arg Asn Ala Phe Ser
 136 35 40 45
 137 Val Tyr Ile Leu Asn Leu Ala Leu Ala Asp Phe Phe Phe Leu Leu Gly
 138 50 55 60
 139 His Ile Ile Asp Ser Ile Leu Leu Leu Asn Val Phe Tyr Pro Ile
 140 65 70 75 80
 141 Thr Phe Leu Leu Cys Phe Tyr Thr Ile Met Met Val Leu Tyr Ile Ala
 142 85 90 95
 143 Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val
 144 100 105 110
 145 Leu Cys Pro Ile Trp Tyr His Cys His Arg Pro Glu His Thr Ser Thr
 146 115 120 125
 147 Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile Leu
 148 130 135 140
 149 Asn Ser Tyr Phe Cys Gly Phe Leu Asn Thr Gln Tyr Lys Asn Glu Asn
 150 145 150 155 160
 151 Gly Cys Leu Ala Leu Asn Phe Phe Thr Ala Ala Tyr Leu Met Phe Leu
 152 165 170 175
 153 Phe Val Val Leu Cys Leu Ser Ser Leu Ala Leu Val Ala Arg Leu Phe
 154 180 185 190
 155 Cys Gly Thr Gly Gln Ile Lys Leu Thr Arg Leu Tyr Val Thr Ile Ile
 156 195 200 205
 157 Leu Ser Ile Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile His
 158 210 215 220
 159 Trp Phe Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Phe Asp Leu
 160 225 230 235 240
 161 Gly Phe Tyr Leu Ala Ser Val Val Leu Thr Ala Ile Asn Ser Cys Ala
 162 245 250 255
 163 Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg His Arg Leu Lys
 164 260 265 270
 165 His Gln Thr Leu Lys Met Val Leu Gln Asn Ala Leu Gln Asp Thr Pro
 166 275 280 285
 167 Glu Thr Ala Lys Ile Met Val Glu Met Ser Arg Ser Lys Ser Glu Pro
 168 290 295 300
 171 <210> SEQ ID NO: 3
 172 <211> LENGTH: 1234
 173 <212> TYPE: DNA
 174 <213> ORGANISM: Mus musculus
 176 <220> FEATURE:
 177 <221> NAME/KEY: CDS
 178 <222> LOCATION: (137)...(1051)
 180 <400> SEQUENCE: 3
 181 tctgtatgtca ctgttatcttt ctttctacac aagccagtga gctacatcca acaagaggat 60
 182 tggggaaagc aatggtaag catttttgc cttaagacc tcagcctcac caacagcacc 120
 183 agtgacaaca aatcca atg gac gaa acc ctc cct gga agt atc aac att agg 172
 184 Met Asp Glu Thr Leu Pro Gly Ser Ile Asn Ile Arg

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Input Set : A:\CALTE004C1seqlist.txt
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185	1	5	10	
187	att ctg atc cca aaa ttg atg atc atc atc ttc gga ctg gtc gga ctg			220
188	Ile Leu Ile Pro Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu			
189	15	20	25	
191	atg gga aac gcc att gtg ttc tgg ctc ctg ggc ttc cac ttg cgc aag			268
192	Met Gly Asn Ala Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys			
193	30	35	40	
195	aat gac ttc tca ctc tac atc cta aac ttg gcc cggt gct gac ttc ctt			316
196	Asn Asp Phe Ser Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu			
197	45	50	55	60
199	tcc ctc ctc agt agt atc ata gct tcc acc ctg ttt ctt ctc aaa gtt			364
200	Phe Leu Leu Ser Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val			
201	65	70	75	
203	tcc tac ctc agc atc atc ttt cac ttg tgc ttt aac acc att atg atg			412
204	Ser Tyr Leu Ser Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met			
205	80	85	90	
207	gtt gtc tac atc aca ggg ata agc atg ctc agt gcc atc agc act gag			460
208	Val Val Tyr Ile Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu			
209	95	100	105	
211	tgc tgc ctg tct gtc ctg ccc acc tgg tat cgc tgc cac cgt cca			508
212	Cys Cys Leu Ser Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro			
213	110	115	120	
215	gta cat aca tca act gtc atg tgt gct gtg atc tgg gtc cta tcc ctg			556
216	Val His Thr Ser Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu			
217	125	130	135	140
219	ttg atc tgc att ctg aat agc tat ttc tgt gct gtc tta cat acc aga			604
220	Leu Ile Cys Ile Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg			
221	145	150	155	
223	tat gat aat gac aat gag tgt ctg gca act aac atc ttt acc gcc tcg			652
224	Tyr Asp Asn Asp Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser			
225	160	165	170	
227	tac atg ata ttt ttg ctt gtg gtc ctc tgt ctg tcc agc ctg gct ctg			700
228	Tyr Met Ile Phe Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu			
229	175	180	185	
231	ctg gcc agg ttg ttc tgt ggc gct ggg cag atg aag ctt acc aga ttt			748
232	Leu Ala Arg Leu Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe			
233	190	195	200	
235	cat gtg acc atc ttg ctg acc ctt ttg gtt ttt ctc ctc tgc ggg ttg			796
236	His Val Thr Ile Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu			
237	205	210	215	220
239	ccc ttt gtc atc tac tgc atc ctg tta ttc aag att aag gat gat ttc			844
240	Pro Phe Val Ile Tyr Cys Ile Leu Leu Phe Lys Ile Lys Asp Asp Phe			
241	225	230	235	
243	cat gta tta gat gtt aat ttt tat cta gca tta gaa gtc ctg act gct			892
244	His Val Leu Asp Val Asn Phe Tyr Leu Ala Leu Glu Val Leu Thr Ala			
245	240	245	250	
247	att aac agc tgt gcc aac ccc atc atc tac ttc ttc gtg ggc tct ttc			940
248	Ile Asn Ser Cys Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe			
249	255	260	265	

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251 aga cat cag ttg aag cac cag acc ctc aaa atg gtt ctc cag agt gca 988
 252 Arg His Gln Leu Lys His Gln Thr Leu Lys Met Val Leu Gln Ser Ala
 253 270 275 280
 255 ctg cag gag act cct gag aca gct gaa aac atg gta gag atg tca agt 1036
 256 Leu Gln Asp Thr Pro Glu Thr Ala Glu Asn Met Val Glu Met Ser Ser
 257 285 290 295 300
 259 aac aaa gca gag cct/tgatgaagag cctctacctg gacctcagag gtggcttg 1091
 260 Asn Lys Ala Glu Pro
 261 305
 263 agtgaggact gccctgtgc acttgaccac tgtccactct tactctagct tactgatttg 1151
 264 acatgcctca gtggtccacc aacaacttca acatctctcc actaacttag tttttctacc 1211
 265 cctcctgaat aaaagcattc atc 1234
 267 <210> SEQ ID NO: 4
 268 <211> LENGTH: 305
 269 <212> TYPE: PRT
 270 <213> ORGANISM: Mus musculus
 272 <400> SEQUENCE: 4
 273 Met Asp Glu Thr Leu Pro Gly Ser Ile Asn Ile Arg Ile Leu Ile Pro
 274 1 5 10 15
 275 Lys Leu Met Ile Ile Ile Phe Gly Leu Val Gly Leu Met Gly Asn Ala
 276 20 25 30
 277 Ile Val Phe Trp Leu Leu Gly Phe His Leu Arg Lys Asn Asp Phe Ser
 278 35 40 45
 279 Leu Tyr Ile Leu Asn Leu Ala Arg Ala Asp Phe Leu Phe Leu Leu Ser
 280 50 55 60
 281 Ser Ile Ile Ala Ser Thr Leu Phe Leu Leu Lys Val Ser Tyr Leu Ser
 282 65 70 75 80
 283 Ile Ile Phe His Leu Cys Phe Asn Thr Ile Met Met Val Val Tyr Ile
 284 85 90 95
 285 Thr Gly Ile Ser Met Leu Ser Ala Ile Ser Thr Glu Cys Cys Leu Ser
 286 100 105 110
 287 Val Leu Cys Pro Thr Trp Tyr Arg Cys His Arg Pro Val His Thr Ser
 288 115 120 125
 289 Thr Val Met Cys Ala Val Ile Trp Val Leu Ser Leu Leu Ile Cys Ile
 290 130 135 140
 291 Leu Asn Ser Tyr Phe Cys Ala Val Leu His Thr Arg Tyr Asp Asn Asp
 292 145 150 155 160
 293 Asn Glu Cys Leu Ala Thr Asn Ile Phe Thr Ala Ser Tyr Met Ile Phe
 294 165 170 175
 295 Leu Leu Val Val Leu Cys Leu Ser Ser Leu Ala Leu Leu Ala Arg Leu
 296 180 185 190
 297 Phe Cys Gly Ala Gly Gln Met Lys Leu Thr Arg Phe His Val Thr Ile
 298 195 200 205
 299 Leu Leu Thr Leu Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Val Ile
 300 210 215 220
 301 Tyr Cys Ile Leu Leu Phe Lys Ile Lys Asp Asp Phe His Val Leu Asp
 302 225 230 235 240
 303 Val Asn Phe Tyr Leu Ala Leu Glu Val Leu Thr Ala Ile Asn Ser Cys
 304 245 250 255

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/849,869

DATE: 05/17/2001
TIME: 08:54:45

Input Set : A:\CALTE004C1seqlist.txt
Output Set: N:\CRF3\05172001\I849869.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date